

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH  
HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)  
Subject: gi|4557225 ref|NP\_000005.1| alpha-2-macroglobulin precursor sp|P01023|A2MG\_HUMAN ALPHA-2-MACROGLOBULIN  
PRECURSOR (ALPHA-2-M) pir||MAHU alpha-2-macroglobulin precursor - human >gb|AAA51551.1| (M11313) alpha-2-macroglobulin  
precursor [Homo sapiens] (SEQ ID NO: 23)  
Length = 1474

Score = 2714 (960.4 bits), Expect = 1.7e-281, P = 1.7e-281  
Identities = 596/1494 (39%), Positives = 874/1494 (58%)

Query: 13 LLLGMLALSPAIAEELPNVLTLPARLNPFSVQKVCLDLSPGYSDVKFTVTLETCKDTQK 192  
          LLL +L +++ + P Y+V +P+ L+ + +K C+ LS V + +LE+ +  
Sbjct: 14 LLLVLLPTDASVSGK-PQYMLVLPSSLJHTTETTEKGCVLLSYLNETVTVSASLESVRGNRS 72

Query: 193 LLEYSGLKKRHLHCISFLVPPAGGTEEVATIRVSGVGNNISFEEKKKVLIQRQNGTFV 372  
          L + LHC++F VP + EEV + V G F+++ V+++ + + FV  
Sbjct: 73 LFTDEAENDVLHCVAFAVK--SSNEEVNFLTIVQKGTQEFKKRTTVMVKNEDSLFV 131

Query: 373 QTDKPLYTPGQQVYFRIVTMDSNFVNDKYSMVLELQDPNSNRIQAQWLEVVPEQGIVDLS 552  
          QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIQAW E G+ S  
Sbjct: 132 QTDKSIYKPGQTVKFRVVSMDNFHPLNELPLVYIQDPKNRIQAQWQSFQLEGGKQFS 191

Query: 553 FQLAPEAMLGTYTVAE---GKTFGTFSVEEYVLPKFKVEVVEPKELSTVQESFLVKIC 723  
          F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C  
Sbjct: 192 FPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFEVQVTPVKIITILEEEMNVSV 251

Query: 724 CRYTYGKPMLGAVQSVQCQKANTYVREVEREQLPDKCRNLSGQTDKTCGFSAPVDMATF 903  
          YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F  
Sbjct: 252 GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCEKFSGQLNSHGCFYQQVKTVF 309

Query: 904 DLIGVAYSHQINIVATVVEEGTGVAEANATQNIYISPMGSMTFEDTSNFYHNFPPFSGI 1083  
          L Y +++ A + EGT VE Q+ I+ + ++F + + PF G++  
Sbjct: 310 QLRKKEYEMKLHTEAQIQEEGTVVVELTGRQSSEITRTITKLSFVKVDSHFRQGIPIFFGQV 369

Query: 1084 RVRGHDDSFLLKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTELETSGWNGTDVSLGKFQM 1263  
          R+ + N ++F I G + TD +GL F++ T+ GT +++ ++  
Sbjct: 370 RLVDGKGVPIPNKVI-F--IRGNEANYISNATTDHGLVQFSINTTNVMGTSLTVRVNYKD 427

Query: 1264 EDLVNPEQVPRYQNAYLHLRPFYSTRTSFLGTHRLNGPLKCGQPQEVLDVYIDPADA 1443  
          Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++  
Sbjct: 428 RSPCYGYQWVSEEEHAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTQVAHYILNGGTL 487

Fig 1A

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

```

Query: 1444 SPDQEIFSYLIGKSLVMEQKHLNKKKGLKASFSLSLTFTSR LAPDP SLVIYAI PP 1623
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGUKKLSFYLLIMAKGGIVRTGHTGLLVKQEDMKGHFSISIPVKSDIAPVARLLIYAVLP 547

Query: 1624 SGGVVADKIQFSVGMCFDQVSLGFSFSPSQQLPGAEEVLQQAAPGSLCALRAVDSESVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWFDPQLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKVPDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSSTNEKDMYSFLEDMLKAFATNSKIRPKMCPQLQQYEMHGPGLRVGFYESDVNGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVROYFPETWLDLFPIGNSGKEAVHVTVPDALITEMKAMSF 2304
      GH P H VR+YFPETW+WDL + ++G V VTVPD ITEMKA +FC
Sbjct: 716 GHARLVHVEEP-HT---ETVRKYFPETWIMDLVVVNSAGVAEYGVTVPTDITITEMKAGAF 771

Query: 2305 TSQSRGFLSPTVGLTAFKPPFFVDLTLPSVVRGESFRLTATIFNYLKDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLGISSTASLRAFQPPFFVELTMPYSVIRGEAFTLKATVNLNYLPCIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKATHHWNITAVKLGHINFTTSTKILDSNEPCGQKGFVP 2664
      + Q C+Ca+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFVTSABALESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGVASESVSLELPVDIVPDSKAYVTVL 2844
      + GR DT+IKP+LV+PEG+ E T +SLTCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVPEGLEKETTFNSLLCPSGGSEVSEELSLKLPPNVVEESARASVSVL 951

Query: 2845 GKQLEILDSEKRKRMEAAKVWRDINGTALQNLQVMPSGCGEQNMVLFAPLIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYCGCGEQNMVLFAPNIYVLDYL 990

Query: 3025 EKAGLITEEIRSAVGFLFEGYQKELMKHNSYSYAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT E++S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEVKS KAIGYLNLTGYQRQNLNKKHYDGSYSTFGERYGRNGNTWLTAFVTKTFA 1050

```

**Fig. 1B**

# BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

```

Query: 3199 QAQKFIFIDPFNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDDEVSLTAVVTAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAYIFIDEAHITQALIWLSQRQKNGCFRSGSLLNNAIKGVEDEVTL SAYITIAL 1110

Query: 3379 EMGKDVEDPMVSQGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EIPLTVTHFVVRNALFCLE-SAMKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTRSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKKDNSVHWERPQKPKAPVGHFYEPOAPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIIVAWLAKQHNAYGGFSSQTQDTWVALQALAKY-ATTAYMPSEEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSQTQDTWVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWIITKQNAQGGFSSQTQDTWVALHALSKYGAATFRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFOQDTLPNVPGMYTLEASGQGCYVYVQTVLRYNILPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GVY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLQQVSLPELPGEYSMKVTGEGCVLYQTSLKYNILPEKEEPPFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNNMAIVEVKMLSGFSPMEGTNQLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSR+SNMAIVDKMVSGFIPLKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDPLNIYLDLIKNTQTYTFTISQSVLVTNLKPAATIKVVDYVLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVDYV F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSQNTLSLFTFTVLQDVVPRDLKPAIVKVVVDYETDEFAIAY 1463

```

FIG. 1C

# BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)  
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. (SEQ ID NO 24)  
 Length = 1474

Score = 2699 (955.2 bits), Expect = 3.2e-280, P = 3.2e-280  
 Identities = 596/1494 (39%), Positives = 870/1494 (58%)

Query:	13	LLGLMLALSPAIAELPNYLVTLPARLNFPSVQKCLDLSPGYSDVKFTVTLETCKDTQK	192
		LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +	
Sbjct:	13	LLLLVLPTDASVSGKPQYMLVPSLLHTETETKGCVLLSYLNETVTVSASLESVRGNS	72
Query:	193	LLSYGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEKKKVLIIQRQNGTFV	372
		L + LHC++F VP + EEV + V G F+++ V+++ + + FV	
Sbjct:	73	LFTDLAENDVLHCVAFAVPK-SSSEEVFMFLTVQVKGPTQEFKKRTTVMVKNEDSLVFV	131
Query:	373	QTDKPLYTPGQVYFRIVTMDSNFVPVNDKYSMVLELQDPNSNRIQAOWLEVPEQGIVDLS	552
		QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S	
Sbjct:	132	QTDKSIYKPGQTVKFRVSMDFNPHLPLVYIQDPKGNRIQAOWQSFQLEGGKQFS	191
Query:	553	FQLAPEAMLGTYTVAAE--GKTFTGTSVEEYVLPKFKVEVVEPKELSTVQESFLVKIC	723
		F L+ E G+Y V V + G+T F+VEH+VLPKF+V+V PK ++ ++E V +C	
Sbjct:	192	FPLSEPFQGSYKVVVQKSGGTEHPFTVEEFVLPKFEVQVTVPKIITILEEEMNVSV	251
Query:	724	CRYTYGKPMLGAVQVSVCKANTYMYREVEREQLPDKCRNLSGQTDKTCFSAVDMATF	903
		YTYGKP+ G V VS+C+K + E C SGQ + GCF V F	
Sbjct:	252	GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCEKFSQNLNSHGCFYQQVKT	309
Query:	904	DLIGVAYSHQINIVATVVEEGTGV EANATQNIYISPMGSMTFEDTSNFYHPNFPFSGKI	1083
		L Y +++ A + EEGT VE Q+ I+ + ++F + + + PF G++	
Sbjct:	310	QLKRKEYEMKLHTEAQIQEEGTVVVELTGRQSEITRTITKLSFVKVDSHFQGIPIFFGQV	369
Query:	1084	RVRGHDDSFLLKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLETSGMNGTDVSLGKFQM	1263
		R+ + N ++F I G + TD +GL F++ T+ GT +++ ++	
Sbjct:	370	RLVDGKGVPIPNKVIF--IRGNEANYYSNATTDDEHGLVQFSINTNMVMTSLTVRVNYKD	427
Query:	1264	EDLVNPEQVPVRYQNAYLHLRPFYSTRSFLGIHRLNGPLKCGQPQEVLDYIIDPADA	1443
		Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++	
Sbjct:	428	RSPCYGQVWVEEHEAHTAYLVFSPKSFVHLEPMSHELPGHTQTQVQAHYILNGGTL	487
Query:	1444	SPDQETSFYSYLLIGKGLVMQKHLNSKKGLKASFSLSTFTSR LAPDPPLVIYAIFP	1623
		+++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P	
Sbjct:	488	LGLKKLSFYLLIMAKGGIVRTGTGHLVQEDMKGHFSISIPVKSADIAPVARLLIYAVLP	547

Fig. 2A

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH  
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

```

Query: 1624 SGGWADKIQFSVGMCFDNOVSLGFSQQLPGAELVELQLQAAPGSLCALRAVDSESVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFPFWGHYPYQVAEYDQCPVSGPWFPPQPLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIINGITY 655

Query: 1984 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSTNEKDMYSFLEDMGLKAF+NSKIRKPKMCPQLQYEMHGPEGLRVGFYESDVMMGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVRQYFPETWLDLFPFGNSGKEAVHVTVPDAITWKAMSF 2304
      GH P H VR+VF ETW+MDL + ++G V VTVPD ITEWKA +FC
Sbjct: 716 CHARLVHVEEP-HT---ETVRKYFAETWLDLVVNSAGVAEVGVTVPTITEWKAGAFC 771

Query: 2305 TSQSRGFGLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATFNLYLDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLIGISTASLRAFQPFVVELTMPYSVIRGEAFTLKATVLYLPCIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKTHHWNITAVKLGHINFTITKILDSNEPCGGQKGFVP 2664
      + Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPEKEQAPHICANGRQTVSWAVTFKSLGNVNFVSAEALQSQELCGTEVPSVP 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGVASESVSLELPVDIVPDSTKAYVTVL 2844
      + GR DT+IKP+LV+PEG+ E T +SLICP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVPEPEGLEKETTFNSLLCPSGGEVSEELSLKLPNNVVEESARASVVL 951

Query: 2845 GKQLEILDSEKRRRMEAAKVWRDIMGTLQNLQVMPSGCGEQNMVLFAPIIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYCGCGEQNMVLFAPNIYVLQYL 990

Query: 3025 EKAGLLTEEIRSAVGFLEIGYQKELMYKHSNGSYSAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT EI+S+A+G+L GYQ++L YKH +CSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEIKSKAIGYINTGYQRLNYKHGYSYTFGERYGRNQGNWLTAFVLKTF 1050

Query: 3199 QAQKFIIDPKNIQDAIKWMAGNQLPSGCVANVGNLLHTAMKGGVDEVSLETAATAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAVIFIDEAHITQALIWLSQRQKDNCGFRSSGSLINNAIKGGVEDEVLTSAITIAL 1110

```

**Fig. 2B**

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH  
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

```

Query: 3379 EMGKDVDDPMVSGQLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EILLTVTHPVVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDOQAIISGESIYWSQKPTPSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + EP A +VE+T+Y LIA LT +P+ T +++
Sbjct: 1170 LNEEAVKKDNSVHWERPQKPKAPVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIWAWLAKQHNAYGGFSSQTQDTVVALQALAKY-ATTAYMPSEEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSTQ TVVAL AL+KY A T + ++S+ F
Sbjct: 1230 SATNIVKWIITKQNAQGGFSSQTQHTVVVALHALSKYGAATFRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQODTLPNVPGMYTLEASGGQGVYVQTVLRYNILPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCVY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLLQQVSLPELPGEYSMKVTGEGCVYLQTSCLKYNILLPEKEEFFFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNNMAIVEVKMLSGFSPEGTNQLLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRSASNNMAIVDKMVS GFPLKPTVKMLERSNHVSRTE 1409

Query: 4246 FGHTLNIYLDLIKNTQTYTFTISQSVLVTNLKPATIKVVDYVYLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVDY F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSNTQTLSLFTTVLQDVPVRDLKPAIVKVDYDYETDEFAIAEY 1463

```

**FIG. 2C**

# BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH OVOS\_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)  
 Subject: >sp|P20740|OVOS\_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >pir||A20872 ovostatin precursor - chicken  
 >emb|CAA55384.1| (X78801) ovomacroglobulin, ovostatin [Gallus gallus] (SEQ ID NO: 41)  
 length = 1473

Score = 1300 (462.7 bits), Expect = 6.1e-135, Sum P(2) = 6.1e-135  
 Identities = 297/849 (34%), Positives = 457/849 (53%), Frame = +3

Query:	96	VYKFPVSPTRKMAQLLLGLMLALSPAIAEEL-PNYLVTLERLNFPSVQKVCIDLSPGYS	272
		+ F ++ KMW + +L +L L A +E P Y++ +PA L S +VCL	
Sbjct:	9	ILSPFCLTVRKMWLKFILAILLHAAAGKEPEQYVLMVAVLQSDSPSQVCLQFFNLNQ	68
Query:	273	DVKFTVTLETDKTKQLLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFE	452
		+ V LE + E + L C++F++PP + +A I + G +	
Sbjct:	69	TISVRVLEYDTINTTIFEKNITTSNGLQCLNFMIPPVT--SVSLAFISFTAKGTTFDLK	126
Query:	453	EKKKVLIQRQNGTFFVQTDKPLYTPGQQVYFRIVTMDSNFVNDKYSVMVELQDPNSNRI	632
		E++ V+I + FVQTDKP+Y PGQ V FR+V +D NF PV + Y ++ +QDP +NRI	
Sbjct:	127	ERRSVMIWNMESFVQTDKPIYKPGQSVFRVVALDFNFKPVQEMYPLIAVQDPQNNRI	186
Query:	633	AQWLEVVPQGIIVDLISFQLAPEAMLGTYTVAE--G-KTFGTFSEVEEYVLPKFKVEVVE	803
		QW V E IV + F L E +LG Y + V + G +T +F VEEYVLPKF V	
Sbjct:	187	FQWQNTSEINIVQIEFPFLTEEPILGNKYIIVTKKSGERTSHSFLVEEYVLPKFDVTVA	246
Query:	804	PKELSTVQESFLVKICCRYTYGKPMLGAVQSVSCQKANTYVYREVEREQLPDKCRNLSGQ	983
		P L+ + VKIC YTYG+P+ G VQ+SVC+ ++Y R + C++ +	
Sbjct:	247	PGSLTVMDSSELTVKICAVITYGQPVGEKVLQSVCRDFDSYG-----RCKKSPVCQSFTKD	301
Query:	984	TDKTCFSAPVDMATFDLIGYAVSHQINIVATVVEEGTGVEANATQNIYISPMGSMTFE	1163
		D GC S + F+L Y +++ A V E+ ATQ+I I+ M S+ FE	
Sbjct:	302	LDTDGCLSHILSSKVFELNRIGYKRNLDVKAIVTEKEQVCNLTATQISITQVMSSLQFE	361
Query:	1164	DTSNFYHPNFPFSGKIRVRGHDDSLKHLVFLVIYGTNGTFNQTLVTDNNGIAPFTLET	1343
		+ + Y P+ G+I++ D+S + N ++ L + N T N T TD NG+APF++T	
Sbjct:	362	NVDHHRRGIPYFGQIKLVDKDNSPISKNVQLFVNKN--THNFT--TDINGIAPFSIDT	418

Fig 3A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH OVOS\_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

```

Query: 1344 SGWNGTDVSLGKFQMEDLVYNPEQVPRYYQNAVYHLRPFYSTTRSFGLGIHRLNGPLKCG 1523
      S ++SL+ ++ D ++ + Y +A L ++ YS T SF+ I L + CG
Sbjct: 419 SKIFDPELSLKALYKTSQCHSEGWIEPSYDASLSVQRLYSWTSFVRIEPLWKDMSCG 478

Query: 1524 QPQEVLDVYIDPADASPDQEIISFSYLLIGKGSVMQKHLNKKKGLKASFSLSLTFT 1703
      Q + + V Y ++ ++F Y + KG +V+ G+ +N + +F + L
Sbjct: 479 QKRMITVYYIINTEGYEHINIVFYVGMAGKIVLTGEIKVNIQADQ-NGTFMIPLVVN 537

Query: 1704 SRLAPDPSLVIYAIFPSSGGVVADKIQFSVEMCFDNQVSLGSPSQQLPGAELVQLQAAP 1883
      ++AP L++Y + P+ +VAD ++FS+E CF N+V L FS Q L + V L ++AA
Sbjct: 538 EKMAPALRLVYMLHPAKELVADSVRFSEIKCFKKNVQLQFSEKQMLTTSNVSLVIEAAA 597

Query: 1884 GSLCALRAVDSEVLLLRPDRELSNRSVYGMFPFHYQYQVAEYDQCVPVSGPWDFPQPL 2063
      S CA+RAVD+S+LLL+ + ELS ++Y + P Q ++ + D PQ
Sbjct: 598 NSFCAVRAVDKSMILLKSETELSAETIYNLHPI----QDLQYIFNGLNLE---DDPQ-- 648

Query: 2064 IDPMPQGHSS-QRSIIWRPFSFE-GTDLFSFFRDVGLKILSNAKIKKPVDCSH---RSPE 2228
      DP + + +RP S G D++ F RD+G+K +N+KI+P C+ R P
Sbjct: 649 -DPCVSSDDIFHKGLYRPLTSGLGPDVYQFLRDMGMKFFTNKIRQPTVCTRETVRPPS 707

Query: 2229 YSTAMG--AGGHPH-----AFESSTPLHQAEVSQVRQYFPETWLDLFPIGNSGKEAVH 2387
      Y G A H + A E H E +R++FPETW+WD+ I ++GK +V
Sbjct: 708 YFLNAGFTASTHVVKLSAEVAREERGRHILET--IREFFPETWIDILINSTGKASVS 765

Query: 2388 VTVPDAITEWKAMSFCTSQSRGFGLSPTVGLTAFKPPFFVDLTLPYSVVRGESFRLTATIF 2567
      T+PD ITEWKA +FC + GFG+S LTAP+PFFVDLTLPYS++ GE F + A +F
Sbjct: 766 YTIPDTITEWKASAFCEELAGFGMSVPA TLTAQPFFVDLTLPYSIIHGDFLVRANVF 825

Query: 2568 NYLKDCIRV 2594
      NYL CI++
Sbjct: 826 NYLNHCIKI 834

```

**Fig 3B**



# BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)  
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. SEQ ID NO: 24  
 Length = 1474

Score = 1289 (458.8 bits), Expect = 5.6e-134, Sum P(2) = 5.6e-134  
 Identities = 300/834 (35%), Positives = 448/834 (53%), Frame = +3

Query: 141 LLLGMLALSPAIAEELPNVLVTLPARLNFPSVQKVCCLDSPGYSDVKFTVLETKDKTK 320  
 LLL +L + A P Y+V +P+ L+ +K C+ LS V + +LE+ +  
 Sb|ct: 13 LLLLVLVPTDASVSGKPQYMLVLPSSLHTTEKGCVLLSYLNETVTVSASLESVRGNRS 72

Query: 321 LLEYSGLKKRHLHCISFLVPPAGGTEEVATIRVSGVGNNISFEKKKVLIRQNGTFV 500  
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV  
 Sb|ct: 73 LFTDLEAENDVLHCVAFAVPK--SSNEEVMFLLTVQVKPTQEFKKRTTMVKNEDSLVFV 131

Query: 501 QTDKPLYTPGQQVYFRIVTMDNSFVNPVNDKYSMVLEQDPNSNRIQAQWLEVPDQGI 680  
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIQW E G+ S  
 Sb|ct: 132 QTDKSIYKPGQTVKFRVWMDNFHPLNELIPLVYIQDPKGNRIQAQWQSFQLEGGKQFS 191

Query: 681 FQLAPEAMLGTYTWAVAE---GKTFTFSVEEYVLPKFVVEVPKELSTVQESFLVKIC 851  
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ +E V +C  
 Sb|ct: 192 FPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFVQVTVVPKIIITILEEMNV 251

Query: 852 CRYTYGKPMLGAVQVSVQCQKANTYWYREVEREQLPDKCRNLSGQTDKTCGFSAPVDM 1031  
 YTYGKP+ G V VS+C+K + + E C SQG + GCF V F  
 Sb|ct: 252 GLTYGKVPVPGHVTVSICRYSDA--SDCHGEDSQAFCEKFGSQLNSHGCIFYQQVTK 309

Query: 1032 DLIGAYSHQINIVATVVEEGTGVAEANATQNIYISPMGSMTEFDTSNFYHNPFFSG 1211  
 L Y +++ A + EGT VE O+ I+ + ++F + + PF G++  
 Sb|ct: 310 QLKREYEMKLHTEAQIQEEGTVVVELTGRQSSSEITRTITKLSFKVVDSHFRQGI 369

Query: 1212 RVRGHDDSFLLKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLETSGWNGTDVSL 1391  
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++  
 Sb|ct: 370 RLVDGKGVPIPNKVIF--IRGNEANYISNATDEHGLVQFSINTNVMTSLTVRV 427

Query: 1392 EDLVNPEQVPYRYQNAYLHLRPFYSTRTSFLGIHRLNGPLKCGQPQEVLDYIDPADA 1571  
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++  
 Sb|ct: 428 RSPCYQWVSEEEHAAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNG 487

Fig. 4A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH  
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

```

Query: 1572 SPDQEIISFSYLLIGKSLVMGQKHLNKKKGLKASFSLSLTFTSRLAPDPSLVIYAIFP 1751
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPVKSDIAPVARILLIYAVLP 547

Query: 1752 SGGVADKIQFSVEMCFDQVSLGFSFSPSQQLPGAELVQLQAAPGSLCALRAVDSEVLIL 1931
      +G V+ D ++ VE C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCLENKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1932 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCVPVSGPWDFPQPLIDPMPQGHSSQRSIIW 2111
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KDAELSASSVYNLLP-----EKDLTGFFGPLN-DQDDEDCINRHNVIYINGITY 655

Query: 2112 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGAG 2252
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSSTNEKDMYSFLEDMLGKAFNTNSKIRKPKMCPQLQYEMHGPEGLRVGFYESDV-MG 714

Query: 2253 GGHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITENKAMSF 2432
      GH P H VR+YF ETW+WDL + ++G V VTVPD ITEWKA +F
Sbjct: 715 RGHARLVHVEEP-HT---ETVRKYFAETWIWDLVVVNSAGVAEVGVTVPTITENKAGAF 770

Query: 2433 CTSQSRGFGGLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATFNLYLKDCIRV 2594
      C S+ G G+S T L AF+PFV+LT+PYSV+RGE+F L AT+ NYL CIRV
Sbjct: 771 CLSEDAGLGISSTASLRAFQPFVVELTMPYSVIRGEAFTLKATVNLNLYLPKCIRV 824

```

**Fig. 4B**